

[illegible]

RESULT 13
P01-US94-08528-9
Sequence 9, Application P01US9408528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: REFINING AND COMBINATIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 448
CORRESPONDENCE ADDRESS:
ADDRESSEE: BREWBY AND NEWMARK
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: PatonIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: P01US9408528
FILING DATE: 09-SEP-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 02 07 416236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 44,044
REFERENCE/DOCKET NUMBER: MURPHY 2 PCT
TELEPHONE/FAX INFORMATION:
TELEPHONE: 202-628-6197
TELEFAX: 202-737-4528
TELEX: 248634
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 442 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
P01-US94-08528-9

Query Match 22.1% Score 540.5; DR 5; Length 442;
Best Local Similarity 31.6%; Pred. No. 6; Pos 41;
Matches 132; Conservative 67; Mismatches 128; Indels 91; Gaps 14;

QY 45 AVLAALMALIVATVIGNALVLAFLVADSSRTQRIPTFLINLSISLTVGALVETPLVIVY 94
DB 2 AFQITITLLSATVTGNLLVLSIKVNTLKVNNYFLLSLACALLTCTISM-LY--- 57
QY 95 VLTGWTGTRGRLKLVVYVHTLTLSSATRIVLITLKLNVKAVSYNAAGGAGKAVK 154
DB 58 LLEERLALATLADLWALDYVASHAVLELLELTFTVSTVSTVSTVSTVSTVSTV 115
QY 195 KMLVWVLAFLVGLPALSWSLTSLSSTSPGCVAAETLYRMVETLCSTLTETPLVAV 214
DB 116 MGLDNLNSFLVWALVLEWLVKRLMAQVYLOFLSQPLTPTGTAAAFYHPIVVR 175
QY 215 LPTRELTYSVLEERTRGSLKAAHAGHETPLVAGLTPPTPTGWSWQVDEAHVLE 274
DB 176 F---LYMKVYETNR AKRQSRTP ----- 198
QY 275 VAVDAVVALADGAT 341
DB 199 -----GKDS-----SSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 285
QY 445 ELDENVQVLTPTSPPTFPVAVVAVVLTGTPKAVATVHTLTAATVHTVHTVHTV 454
DB 11 KLVDAVKKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA 111
QY 234 KLVDAVKKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA 203
DB 395 ETSVALLWLVDAVHTVAVLGLTHTLTSAA LPTLLTPTLPTLPTLPTLPTLPTL 15

DB 284 FLGTWLTATVATLIDWVATLTKAATLPTLTLTLTLTLTLTLTLTLTLTLTL 111
US 08 118-270-13
RESULT 14
US 08 118-270-13
Sequence 13, Application US 08118270
Patent No. 5508484
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David L.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: REFINING AND COMBINATIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 448
CORRESPONDENCE ADDRESS:
ADDRESSEE: BREWBY AND NEWMARK
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: PatonIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 02 09 216290
FILING DATE: 09-SEP-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 02 07 943246
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 44,044
REFERENCE/DOCKET NUMBER: MURPHY 2A
TELEPHONE/FAX INFORMATION:
TELEPHONE: 202-628-6197
TELEFAX: 202-737-4528
TELEX: 248634
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US 08 118-270-13

Query Match 22.40% Score 5292; DR 17; Length 448;
Best Local Similarity 29.2%; Pred. No. 66; Pos 41;
Matches 122; Conservative 61; Mismatches 119; Indels 98; Gaps 14;

QY 45 AVLAALMALIVATVIGNALVLAFLVADSSRTQRIPTFLINLSISLTVGALVETPLVIVY 94
DB 2 AFQITITLLSATVTGNLLVLSIKVNTLKVNNYFLLSLACALLTCTISM-LY--- 57
QY 95 VLTGWTGTRGRLKLVVYVHTLTLSSATRIVLITLKLNVKAVSYNAAGGAGKAVK 154
DB 58 LLEERLALATLADLWALDYVASHAVLELLELTFTVSTVSTVSTVSTVSTVSTV 115
QY 195 KMLVWVLAFLVGLPALSWSLTSLSSTSPGCVAAETLYRMVETLCSTLTETPLVAV 214
DB 116 MGLDNLNSFLVWALVLEWLVKRLMAQVYLOFLSQPLTPTGTAAAFYHPIVVR 175
QY 215 LPTRELTYSVLEERTRGSLKAAHAGHETPLVAGLTPPTPTGWSWQVDEAHVLE 274
DB 176 F---LYMKVYETNR AKRQSRTP ----- 198
QY 275 VAVDAVVALADGAT 341
DB 199 -----GKDS-----SSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 285
QY 445 ELDENVQVLTPTSPPTFPVAVVAVVLTGTPKAVATVHTLTAATVHTVHTVHTV 454
DB 11 KLVDAVKKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA 111
QY 234 KLVDAVKKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA 203
DB 395 ETSVALLWLVDAVHTVAVLGLTHTLTSAA LPTLLTPTLPTLPTLPTLPTLPTL 15

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in search, using sw model

January 10, 2002, 14:42:50, Search Time: 33.01 Seconds
(without alignment)

S. 09-891-05.1-2.
404
MURRAY PETERMAN ASSOCIATES, INC., 100 HIGHTOWER DRIVE, SUITE 100

$$\text{LCSUM}_2$$

$$\text{apop } 10.0, \text{ Gapext } 0.5$$

19241 SOYS. 7/17/52 records

its satisfying chosen parameters: 219241

[illegible]

Definition 4.1. $\mathcal{H}^1(\mathbb{R}^n)$ is the space of functions f on \mathbb{R}^n such that

Minimum

Maximum Match Length

[illegible]

★
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X
L
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★

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES		
Result	Score	Quality
Ref.	Mean	Length
1	724	30.1
2	596	40.1
3	429514	490
4	596	460
5	596	460
6	596	460
7	596	460
8	596	460
9	596	460
10	596	460
11	596	460
12	596	460
13	596	460
14	596	460
15	596	460
16	596	460
17	596	460
18	596	460
19	596	460
20	596	460
21	596	460
22	596	460
23	596	460
24	596	460
25	596	460
26	596	460
27	596	460
28	596	460
29	596	460

[illegible]

441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

Genome version: 1.5
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EM protein - protein search, using sw model

Run on: January 10, 2002, 14:43:30 : Search time: 23.08 seconds
(without alignments)
701,461 Million cell updates/sec

Perfect score: 2403

Sequence: 1 MERAPPAPAPNAGAAAGAA
1005511P368888E01.453

Scoring table: BLASTSUM62

Gapop 10.0 : Gapext 0.5

Searched: 10059 seqs, 3664827 residues

Total number of hits satisfying chosen parameters: 10059

Minimum DB Seq length: 0

Maximum DB Seq length: 20000000

Post-processing: Minimum Match ok

Maximum Match: 98

Listed First 45 summaries

Database: SwissProt, 98*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	724	30.1	350	1 HHR_HUMAN	95428 homo sapien
2	596.5	24.8	460	1 A2M1_MACMU	P56489 musca mela
3	596	24.8	460	1 A2M1_RAT	P08482 rattus norv
4	595.5	24.8	460	1 A2M1_HUMAN	P11225 homo sapien
5	591.5	24.6	460	1 A2M1_PTC	P04761 sus scrofa
6	584	24.3	460	1 A2M1_MOUSE	P12457 mus muscula
7	556.5	23.2	590	1 A2M1_BOVIN	P41984 bos taurus
8	549.5	22.9	590	1 A2M1_PIG	P11483 sus scrofa
9	547.5	22.9	590	1 A2M1_PIG	P08473 sus scrofa
10	546	22.7	479	1 A2M1_HUMAN	P08173 homo sapien
11	545.5	22.7	590	1 A2M1_HUMAN	P20409 homo sapien
12	545.5	22.7	590	1 A2M1_HUMAN	Q96244 pan troglod
13	545	22.7	590	1 A2M1_PNTY	Q96242 pan troglod
14	541.5	22.5	585	1 A2M1_RAT	P08483 rattus norv
15	539.5	22.3	722	1 A2M1_MOUSE	P56470 musca mela
16	536	22.3	179	1 A2M1_MOUSE	P12211 mus muscula
17	535.5	22.3	572	1 A2M1_HUMAN	P08472 homo sapien
18	533.5	22.2	478	1 A2M1_RAT	P08485 rattus norv
19	533.5	22.2	589	1 A2M1_MOUSE	Q96273 mus muscula
20	529.5	22.0	459	1 A2M1_HUMAN	P08474 homo sapien
21	526.5	21.9	466	1 A2M1_RAT	P10980 rattus norv
22	526.5	21.9	531	1 A2M1_RAT	P08471 rattus norv
23	519.5	21.6	466	1 A2M1_HUMAN	P08472 homo sapien
24	518.5	21.5	466	1 A2M1_HUMAN	P08472 homo sapien
25	517.5	21.5	466	1 A2M1_HUMAN	P08472 homo sapien
26	515	21.4	466	1 A2M1_PTC	P49578 sus scrofa
27	511.5	21.3	466	1 A2M1_PTC	P18479 sus scrofa
28	505.5	21.0	450	1 A2M1_PTC	P18471 sus scrofa
29	505.5	21.0	452	1 A2M1_RAT	P29533 rat norv
30	504	21.0	490	1 A2M1_PTC	P17400 rat norv
31	499.5	20.8	601	1 A2M1_HUMAN	P22470 drosophila
32	496.5	20.7	461	1 A2M1_HUMAN	P18475 homo sapien
33	493	20.5	442	1 A2M1_HUMAN	Q91081 rattus norv

34	492.5	20.4	450	1 A2M1_HUMAN	P08474 homo sapien
35	491.5	20.2	450	1 A2M1_PTC	P18475 homo sapien
36	485	20.2	455	1 A2M1_MOUSE	P56469 homo sapien
37	485	20.2	458	1 A2M1_HUMAN	P22909 rattus norv
38	483.5	20.1	450	1 A2M1_RAT	Q91337 mus muscula
39	481	20.0	458	1 A2M1_MOUSE	P22086 rattus norv
40	481	20.0	458	1 A2M1_RAT	P29404 rattus norv
41	479.5	20.0	474	1 A2M1_MOUSE	Q91476 rattus norv
42	478.5	19.9	455	1 A2M1_PTC	P08475 homo sapien
43	477	19.9	448	1 A2M1_HUMAN	P08544 homo sapien
44	475	19.8	484	1 A2M1_HUMAN	P18099 homo sapien
45	473	19.7	450	1 A2M1_HUMAN	P18099 homo sapien

AL COMMENTS

RESID 1

HHR_HUMAN

10 HHR_HUMAN STANDARD 1913 590 AA.

AC Q96088: Q96088

DT 20 AUG 2001 (Rel. 40, Created)

DI 20 AUG 2001 (Rel. 40, Last sequence update)

DI 20 AUG 2001 (Rel. 40, Last annotation update)

DE HISTAMINE H4 RECEPTOR (HHR4) (HHR4)

GN HHR4

OS Homo sapiens (Human)

OC Eukaryota: Metazoa: Chordata: Mammalia: Vertebrata: Euteleostomi:

OC Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo:

OX NCBI TaxID: 9606

RN 111

RF SEQUENCE FROM N.A.

RX MEDLINE 20539137; PubMed 10473474

KA Li J., Makris N., Sachs T., Hoshino Y., Matsuno S., Li J.

RT "Molecular cloning and characterization of novel type of histamine

receptor preferentially expressed in leukocytes."

RI J. Biol. Chem. 275:36781-36786 (2000).

RN 12

RF SEQUENCE FROM N.A.

RX MEDLINE 20568755; PubMed 11118344

KA Sakurai T., Ishida E., Hibiya Y., Iida M., Inaba K.

RT "Molecular cloning and characterization of a new human histamine

receptor, HHR4."

RI Biochem. Biophys. Res. Commun. 273:615-620 (2000).

RN 14

RF SEQUENCE FROM N.A.

KA Jones P.G., Wu S., Betty M.

RT "Cloning of a novel histamine receptor."

RI Submitted (11-20-01) to the EMBL/GenBank/DBJ databases.

CC FUNCTION: THE H4 SUBTYPE OF HISTAMINE RECEPTOR IS A G-PROTEIN-

COUPLED RECEPTOR THAT MEDIATES THE HISTAMINE SIGNAL IN PERIPHERAL TISSUES.

CC SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC TISSUE SPECIFICITY: IS EXPRESSED IN A WIDE VARIETY OF PERIPHERAL

TISSUES, INCLUDING THE BRAIN, LIVER, KIDNEY, LUNG, EMBRYO, LIVER, PAN-

CREAS, SKIN, MUSCLE, BLOOD, TESTIS, FETAL LIVER, SMALL INTESTINE, STOM-

ACH, FETAL LIVER AND UTERI NODE.

CC SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC THIS SWISS-PROT entry is copyrighted. It is produced through a collaboration

between the Swiss Institute of Bioinformatics and the EMBL database.

CC the European Bioinformatics Institute. There are no restrictions on its

use by non-profit institutions as long as the source is acknowledged.

CC modified and this statement is hereby acknowledged by and for EMBL

on 11-20-01. It is a legal deposit of the EMBL archive.

CC or send an email to help@ebi.ac.uk for more information.

CC

DR HHR4: A06419.1; RefSeq: NM_001001001

DR HHR4: A06419.1; RefSeq: NM_001001001

DR HHR4: A06419.1; RefSeq: NM_001001001

DR HHR4: A06419.1; RefSeq: NM_001001001

DR HHR4: A06419.1; RefSeq: NM_001001001

PRESITE: PS50262; G-protein coupled receptor; Glycoprotein; G-protein coupled receptor; Transmembrane; Palmitate; Domain; TRANSMEM 1 19; EXTRACELLULAR (POTENTIAL); TRANSMEM 20 40; TRANSMEM 41 52; CYTOPLASMIC (POTENTIAL); TRANSMEM 53 73; TRANSMEM 74 87; EXTRACELLULAR (POTENTIAL); TRANSMEM 88 108; TRANSMEM 109 131; CYTOPLASMIC (POTENTIAL); TRANSMEM 132 152; TRANSMEM 153 172; EXTRACELLULAR (POTENTIAL); TRANSMEM 173 193; TRANSMEM 194 304; CYTOPLASMIC (POTENTIAL); TRANSMEM 305 425; TRANSMEM 426 441; EXTRACELLULAR (POTENTIAL); TRANSMEM 442 462; TRANSMEM 463 490; CYTOPLASMIC (POTENTIAL); TRANSMEM 491 507; BY SIMILARITY; TRANSMEM 508 516; N-LINKED (GLNAC...) (POTENTIAL); TRANSMEM 517 525; N-LINKED (GLNAC...) (POTENTIAL); TRANSMEM 526 534; PALMITATE (POTENTIAL); TRANSMEM 535 543; PALMITATE (POTENTIAL); TRANSMEM 544 552; PALMITATE (POTENTIAL); TRANSMEM 553 561; PALMITATE (POTENTIAL); TRANSMEM 562 570; PALMITATE (POTENTIAL); TRANSMEM 571 579; PALMITATE (POTENTIAL); TRANSMEM 580 588; PALMITATE (POTENTIAL); TRANSMEM 589 597; PALMITATE (POTENTIAL); TRANSMEM 598 606; PALMITATE (POTENTIAL); TRANSMEM 607 615; PALMITATE (POTENTIAL); TRANSMEM 616 624; PALMITATE (POTENTIAL); TRANSMEM 625 633; PALMITATE (POTENTIAL); TRANSMEM 634 642; PALMITATE (POTENTIAL); TRANSMEM 643 651; PALMITATE (POTENTIAL); TRANSMEM 652 660; PALMITATE (POTENTIAL); TRANSMEM 661 669; PALMITATE (POTENTIAL); TRANSMEM 670 678; PALMITATE (POTENTIAL); TRANSMEM 679 687; PALMITATE (POTENTIAL); TRANSMEM 688 696; PALMITATE (POTENTIAL); TRANSMEM 697 705; PALMITATE (POTENTIAL); TRANSMEM 706 714; PALMITATE (POTENTIAL); TRANSMEM 715 723; PALMITATE (POTENTIAL); TRANSMEM 724 732; PALMITATE (POTENTIAL); TRANSMEM 733 741; PALMITATE (POTENTIAL); TRANSMEM 742 750; PALMITATE (POTENTIAL); TRANSMEM 751 759; PALMITATE (POTENTIAL); TRANSMEM 760 768; PALMITATE (POTENTIAL); TRANSMEM 769 777; PALMITATE (POTENTIAL); TRANSMEM 778 786; PALMITATE (POTENTIAL); TRANSMEM 787 795; PALMITATE (POTENTIAL); TRANSMEM 796 804; PALMITATE (POTENTIAL); TRANSMEM 805 813; PALMITATE (POTENTIAL); TRANSMEM 814 822; PALMITATE (POTENTIAL); TRANSMEM 823 831; PALMITATE (POTENTIAL); TRANSMEM 832 840; PALMITATE (POTENTIAL); TRANSMEM 841 849; PALMITATE (POTENTIAL); TRANSMEM 850 858; PALMITATE (POTENTIAL); TRANSMEM 859 867; PALMITATE (POTENTIAL); TRANSMEM 868 876; PALMITATE (POTENTIAL); TRANSMEM 877 885; PALMITATE (POTENTIAL); TRANSMEM 886 894; PALMITATE (POTENTIAL); TRANSMEM 895 903; PALMITATE (POTENTIAL); TRANSMEM 904 912; PALMITATE (POTENTIAL); TRANSMEM 913 921; PALMITATE (POTENTIAL); TRANSMEM 922 930; PALMITATE (POTENTIAL); TRANSMEM 931 939; PALMITATE (POTENTIAL); TRANSMEM 940 948; PALMITATE (POTENTIAL); TRANSMEM 949 957; PALMITATE (POTENTIAL); TRANSMEM 958 966; PALMITATE (POTENTIAL); TRANSMEM 967 975; PALMITATE (POTENTIAL); TRANSMEM 976 984; PALMITATE (POTENTIAL); TRANSMEM 985 993; PALMITATE (POTENTIAL); TRANSMEM 994 1002; PALMITATE (POTENTIAL); TRANSMEM 1003 1011; PALMITATE (POTENTIAL); TRANSMEM 1012 1020; PALMITATE (POTENTIAL); TRANSMEM 1021 1029; PALMITATE (POTENTIAL); TRANSMEM 1030 1038; PALMITATE (POTENTIAL); TRANSMEM 1039 1047; PALMITATE (POTENTIAL); TRANSMEM 1048 1056; PALMITATE (POTENTIAL); TRANSMEM 1057 1065; PALMITATE (POTENTIAL); TRANSMEM 1066 1074; PALMITATE (POTENTIAL); TRANSMEM 1075 1083; PALMITATE (POTENTIAL); TRANSMEM 1084 1092; PALMITATE (POTENTIAL); TRANSMEM 1093 1101; PALMITATE (POTENTIAL); TRANSMEM 1102 1110; PALMITATE (POTENTIAL); TRANSMEM 1111 1119; PALMITATE (POTENTIAL); TRANSMEM 1120 1128; PALMITATE (POTENTIAL); TRANSMEM 1129 1137; PALMITATE (POTENTIAL); TRANSMEM 1138 1146; PALMITATE (POTENTIAL); TRANSMEM 1147 1155; PALMITATE (POTENTIAL); TRANSMEM 1156 1164; PALMITATE (POTENTIAL); TRANSMEM 1165 1173; PALMITATE (POTENTIAL); TRANSMEM 1174 1182; 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PALMITATE (POTENTIAL); TRANSMEM 2028 2036; PALMITATE (POTENTIAL); TRANSMEM 2037 2045; PALMITATE (POTENTIAL); TRANSMEM 2046 2054; PALMITATE (POTENTIAL); TRANSMEM 2055 2063; PALMITATE (POTENTIAL); TRANSMEM 2064 2072; PALMITATE (POTENTIAL); TRANSMEM 2073 2081; PALMITATE (POTENTIAL); TRANSMEM 2082 2090; PALMITATE (POTENTIAL); TRANSMEM 2091 2099; PALMITATE (POTENTIAL); TRANSMEM 2100 2108; PALMITATE (POTENTIAL); TRANSMEM 2109 2117; PALMITATE (POTENTIAL); TRANSMEM 2118 2126; PALMITATE (POTENTIAL); TRANSMEM 2127 2135; PALMITATE (POTENTIAL); TRANSMEM 2136 2144; PALMITATE (POTENTIAL); TRANSMEM 2145 2153; PALMITATE (POTENTIAL); TRANSMEM 2154 2162; PALMITATE (POTENTIAL); TRANSMEM 2163 2171; PAL

FT	DOMAIN	170	191	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	192	214	5 (POTENTIAL).
FT	DOMAIN	215	443	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	444	464	6 (POTENTIAL).
FT	DOMAIN	465	478	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	479	498	7 (POTENTIAL).
FT	DOMAIN	499	542	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	8	8	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	103	183	BY SIMILARITY.
FT	MOD_RES	501	501	PHOSPHORYLATION (POTENTIAL).
FT	MOD_RES	505	505	PHOSPHORYLATION (POTENTIAL).
SEQ	SEQUENCE	532 AA.	66140 MW	33KCF6D7E600D79 CRC64
Query Match				
Best Local Similarity 22.48; Score 536.5; DB 1; Length 542;				
Matches 145; Conservative 81; Mismatches 169; Indels 147; Gaps 13;				
QY	43 WTAV-LAALMALLVATVYGLCHALVMIATVANSLSLTGRTTTLRLATGSLVGLATGLTPLY	91		
DB	28 MEVLSIAAVTAVVSLTFLVGRVLMELSHVNSQLKVMNYGLSLACAGLITGLTSMNLY	87		
QY	92 VYVVLGRWFGKGLCKLVVYGLTSSAFNVLVSYDFELSVTRAVSYRAQGDPTTR	151		
DB	88 TTYTLGRWALSLADIMALDYVANSNVMNLLVTSDFYFTTIRPTTYRAKRTPKRA	147		
QY	152 AVRKMLVWLAFLLYGPALLSWEXYSGSSITFGHGYAFEFYNNWYELLITASLLEFETPE	211		
DB	148 GV-MGLAMLSFLWAPALLWQVVIWKRTVPLDRLQQLFSEPTTTCGTALAAPYTPV	206		
QY	212 LSVTFENLSLYNLTORRTKLRLGKRAEACDEPPPAQSPPPP	261		
DB	207 SVBTL	LYRTFLRTKRTKRLALQWSSSVTFARFKRAHRALEKSELTETPTTLA	262	
QY	262 -----WQKHGEMPLHRYGVGGAAGACAGATLGGGGGSGSVASPTSSSSSSSSSG	313		
DB	263 QREDRFTSKSSSK	KASISGRPSGATLSTNCAKAAQLTCSSTPSSED	311	
QY	314 TEPDS-	LEPDSKP	334	
DB	312 DRTATLAVLAVYKSKSKSKSESSSLALKEFLVKAQTEAHDSLTUNYELSPAAAHBP	371		
QY	345 KHKMWVSQSP	-----TQPER	449	
DB	373 KQKAVATFELVAVVAGLQAGKAGHAKVIMNSLVASLSPSLNENSHLMREER	431		
QY	450 ---SPDPVPAPSLAVVSTELHONATVLEHTEAACHGVYTGWTETTELWAKASAV	467		
DB	442 MVLKERRAAQTLATLAFITWTPTNIMVLVSTPC-DKCVPTVIMHILGYWLVVNSIV	490		
QY	408 DIVLYLTHETKATFELGLQKLEAGHSLLEK	WKARK	448	
DB	491 RPDVATGHFTFFFTFPPT	FEWERK	518	

Search completed: January 10, 2002, 14:46:18
Job time: 448 sec

Best Local Similarity		88.6%	Prd. B.	1.5x	17%	
Matches 1209:		Conserved	97	Mismatches	150	Gaps
QY	243	500	500	0	0	0
DB	1387	500	500	0	0	0
QY	405	500	500	0	0	0
DB	470	500	500	0	0	0
QY	463	500	500	0	0	0
DB	469	500	500	0	0	0
QY	423	500	500	0	0	0
DB	429	500	500	0	0	0
QY	422	500	500	0	0	0
DB	489	500	500	0	0	0
QY	482	500	500	0	0	0
DB	549	500	500	0	0	0
QY	542	500	500	0	0	0
DB	609	500	500	0	0	0
QY	602	500	500	0	0	0
DB	609	500	500	0	0	0
QY	662	500	500	0	0	0
DB	729	500	500	0	0	0
QY	722	500	500	0	0	0
DB	789	500	500	0	0	0
QY	762	500	500	0	0	0
DB	849	500	500	0	0	0
QY	842	500	500	0	0	0
DB	909	500	500	0	0	0
QY	902	500	500	0	0	0
DB	969	500	500	0	0	0
QY	962	500	500	0	0	0
DB	1029	500	500	0	0	0
QY	1022	500	500	0	0	0
DB	1086	500	500	0	0	0
QY	1075	500	500	0	0	0
DB	1146	500	500	0	0	0
QY	1139	500	500	0	0	0
DB	1206	500	500	0	0	0
QY	1199	500	500	0	0	0
DB	1266	500	500	0	0	0
QY	1259	500	500	0	0	0
DB	1326	500	500	0	0	0
QY	1319	500	500	0	0	0
DB	1399	500	500	0	0	0

BB	1429	500	500	0	0	0
QY	1439	500	500	0	0	0
DB	1486	500	500	0	0	0
QY	1489	500	500	0	0	0
DB	1509	500	500	0	0	0
QY	1509	500	500	0	0	0
DB	1569	500	500	0	0	0
QY	1569	500	500	0	0	0
DB	1626	500	500	0	0	0
QY	1604	500	500	0	0	0
DB	1671	500	500	0	0	0
RESULT	9					
ARI04203						
DEFINITION	Sequence 4 from patient US 6095545.					
ACCESSION	ARI04203					
VERSION	ARI04203.1					
KEYWORDS	Sequence					
SOURCE	GenBank					
FEATURES	Location/Qualifiers					
REMARKS	OneLassified.					
AUTHORS	Golden, L.A.D., and G. K. Smith, R. Alexandru.					
TITLE	Methods for detecting nucleic acid molecules encoding a member of the muscarinic family of receptors					
JOURNAL	Patent: US 6095545-A 4 21 00; 2000					
FEATDES	Location/Qualifiers					
BASE	609 a	1552 c	603 g	680 t		
ORIGIN						
Query Match	53.3%	Score 1094	DB 6	Length 3244		
Best Local Similarity	88.6%	Prd. No. 1.5x-17%				
Matches 1209:	Conserved	97	Mismatches	150	Gaps	23
QY	243	500	500	0	0	0
DB	750	500	500	0	0	0
QY	405	500	500	0	0	0
DB	470	500	500	0	0	0
QY	463	500	500	0	0	0
DB	469	500	500	0	0	0
QY	423	500	500	0	0	0
DB	429	500	500	0	0	0
QY	422	500	500	0	0	0
DB	489	500	500	0	0	0
QY	482	500	500	0	0	0
DB	549	500	500	0	0	0
QY	542	500	500	0	0	0
DB	609	500	500	0	0	0
QY	602	500	500	0	0	0
DB	609	500	500	0	0	0
QY	662	500	500	0	0	0
DB	729	500	500	0	0	0
QY	722	500	500	0	0	0
DB	789	500	500	0	0	0
QY	762	500	500	0	0	0
DB	849	500	500	0	0	0
QY	842	500	500	0	0	0
DB	909	500	500	0	0	0
QY	902	500	500	0	0	0
DB	969	500	500	0	0	0
QY	962	500	500	0	0	0
DB	1029	500	500	0	0	0
QY	1022	500	500	0	0	0
DB	1086	500	500	0	0	0
QY	1075	500	500	0	0	0
DB	1146	500	500	0	0	0
QY	1139	500	500	0	0	0
DB	1206	500	500	0	0	0
QY	1199	500	500	0	0	0
DB	1266	500	500	0	0	0
QY	1259	500	500	0	0	0
DB	1326	500	500	0	0	0
QY	1319	500	500	0	0	0
DB	1399	500	500	0	0	0


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DB 61 VASGSLGQRRFTLLRLALSLGLAVNFTTLLVYVTLVGLDARTGRLGRLKALVAVLLLT 129
QY 120 ASAPVAVIETLRLSVTKAVSYAGAGLTLRFAVERPRLVAVIATLTYDGLTAWT 129
DB 111 LLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLL 129
DB 121 SSVNIVLISYDRLSVTRVSYRAGQGLTRAVKRVKLVVWVLAFLYGLALLSWEYLSS 180
QY 180 GSSIFEPHETAEFFRWYFELTASTDEFFDPLSVDFPGSYLMLDRLRRLRGLZAKAA 200
DB 181 GSSIFEPHETAEFFRWYFELTASTDEFFDPLSVDFPGSYLMLDRLRRLRGLZAKAA 240
QY 240 ASPTVETAEAGSETPLDQWYVWLEKQVANDVSAIVDAAVZALAAALGAGLGLAA 299
DB 111 LLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLL 299
DB 241 APTVETAEAGSSQPTDQWYVWLEKQVANDVSAIVDAAVZALAAALGAGLGLAA 303SS 298
QY 299 VASPTVETAEAGSETPLDQWYVWLEKQVANDVSAIVDAAVZALAAALGAGLGLAA 359
DB 299 AASPTVETAEAGSETPLDQWYVWLEKQVANDVSAIVDAAVZALAAALGAGLGLAA 374
QY 359 SLAVVSTPLGLWAPYLLRLTRAAQRGQVDFDQWYFELSLWLVWANSVAVNIVAVTALD 419
DB 359 SLAVVSTPLGLWAPYLLRLTRAAQRGQVDFDQWYFELSLWLVWANSVAVNIVAVTALD 419
QY 419 PRGATPLDQWYFELSLWLVWANSVAVNIVAVTALD 419
DB 111 LLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLL 419
DB 419 PRGATPLDQWYFELSLWLVWANSVAVNIVAVTALD 419

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RESULT 6
QYQYNT7 PRELIMINARY: PRI: 413 AA.
AC QYQYNT7
DI 01-MAY-2000 (TEMPREL, 15, Created)
DI 01-MAY-2000 (TEMPREL, 15, last sequence update)
DI 01-JUN-2001 (TEMPREL, 17, last annotation update)
DE G PROTEIN COUPLED RECEPTOR (HISTAMINE H3 RECEPTOR HAS ISSUES)
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_taxid 10116;
RN 111
RF SEQUENCE FROM R.A.
RA Tadani H., Takamura T., Nakamura I., Ohta M.:
RI "Cloning of a novel G protein coupled receptor."
RI Submitted (unpubl) to the Exp. Med. Lab. database
[2]
SEQUENCE FROM N.A.
RA Morisset S., Rouleau A., Liqueur X., Chabon F., Tardivel-Lacrambe J.,
RA Stark H., Schumack W., Garelle R.G., Schwartz J.C., Attard J. M.,
RI "High constitutive activity of the rat histamine H3 receptor."
RN 121
RL Nature 010-0(2001).
RL EMBL: AB015646; BAA88767.1;
RL EMBL: AY009471; AAK32370.1;
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR InterPro: IPR004980; H3_histamine_rec.
DR Pfam: PF00001; 7tm1.1;
DR PRINTS: PR03237; GPCR_Rhodopsin.
DR PRINTS: PR01471; HISTAMINEH3R.
DR PROSITE: PS02627; G_PROTEIN_RECEP_F1_1; UNKN_WN_1.
DR PROSITE: PS02627; G_PROTEIN_RECEP_F1_2;
KW Receptor.
SQ SEQUENCE 413 AA; 45888 MW; 71995CFD1CDHAK6C0 CR664;

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Query Match 85.76; Score 2060; DB 11; Length 413;
Best local Similarity 88.19; Pred. No. 2,6c-143;
Matches 393; Conservative 7; Mismatches 12; Indels 34; Gaps 60
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DB 1 MURAPPDGLMNASGLAGEAAAGARQFSAAVAVLAALMALLIVATVLAALVMAFV 60
QY 61 ADSLSRTQNNFFLENAISDFLVCAAPPLDLYVVPVVLTRGWRPSCRLQKRLVAVVLLAT 120
DB 111 LLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLL 120

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DB 61 ASAPVAVIETLRLSVTKAVSYAGAGLTLRFAVERPRLVAVIATLTYDGLTAWT 129
QY 120 ASAPVAVIETLRLSVTKAVSYAGAGLTLRFAVERPRLVAVIATLTYDGLTAWT 180
DB 111 LLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLL 180
DB 121 SSVNIVLISYDRLSVTRVSYRAGQGLTRAVKRVKLVVWVLAFLYGLALLSWEYLSS 180
QY 180 GSSIFEPHETAEFFRWYFELTASTDEFFDPLSVDFPGSYLMLDRLRRLRGLZAKAA 240
DB 181 GSSIFEPHETAEFFRWYFELTASTDEFFDPLSVDFPGSYLMLDRLRRLRGLZAKAA 240
QY 240 ASPTVETAEAGSETPLDQWYVWLEKQVANDVSAIVDAAVZALAAALGAGLGLAA 299
DB 111 LLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLL 299
DB 241 APTVETAEAGSSQPTDQWYVWLEKQVANDVSAIVDAAVZALAAALGAGLGLAA 303SS 299
QY 299 VASPTVETAEAGSETPLDQWYVWLEKQVANDVSAIVDAAVZALAAALGAGLGLAA 359
DB 299 AASPTVETAEAGSETPLDQWYVWLEKQVANDVSAIVDAAVZALAAALGAGLGLAA 374
QY 359 SLAVVSTPLGLWAPYLLRLTRAAQRGQVDFDQWYFELSLWLVWANSVAVNIVAVTALD 419
DB 359 SLAVVSTPLGLWAPYLLRLTRAAQRGQVDFDQWYFELSLWLVWANSVAVNIVAVTALD 419
QY 419 PRGATPLDQWYFELSLWLVWANSVAVNIVAVTALD 419
DB 111 LLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLL 419
DB 419 PRGATPLDQWYFELSLWLVWANSVAVNIVAVTALD 419

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RESULT 7
QYQYNT7 PRELIMINARY: PRI: 413 AA.
AC QYQYNT7
DI 01-MAY-2000 (TEMPREL, 15, Created)
DI 01-MAY-2000 (TEMPREL, 15, last sequence update)
DI 01-JUN-2001 (TEMPREL, 17, last annotation update)
DE HISTAMINE H3 RECEPTOR HAS ISSUES
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_taxid 10116;
RN 111
RF SEQUENCE FROM R.A.
RA Tadani H., Takamura T., Nakamura I., Ohta M.:
RI "Cloning of a novel G protein coupled receptor."
RI Submitted (unpubl) to the Exp. Med. Lab. database
[2]
SEQUENCE FROM N.A.
RA Morisset S., Rouleau A., Liqueur X., Chabon F., Tardivel-Lacrambe J.,
RA Stark H., Schumack W., Garelle R.G., Schwartz J.C., Attard J. M.,
RI "High constitutive activity of the rat histamine H3 receptor."
RN 121
RL Nature 010-0(2001).
RL EMBL: AB015646; BAA88767.1;
RL EMBL: AY009471; AAK32370.1;
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR InterPro: IPR004980; H3_histamine_rec.
DR Pfam: PF00001; 7tm1.1;
DR PRINTS: PR03237; GPCR_Rhodopsin.
DR PRINTS: PR01471; HISTAMINEH3R.
DR PROSITE: PS02627; G_PROTEIN_RECEP_F1_1; UNKN_WN_1.
DR PROSITE: PS02627; G_PROTEIN_RECEP_F1_2;
KW Receptor.
SQ SEQUENCE 413 AA; 44176 MW; 5470AATPGRDGLT6 CR664;

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Query Match 85.19; Score 2060; DB 11; Length 413;
Best local Similarity 87.79; Pred. No. 2,6c-143;
Matches 393; Conservative 7; Mismatches 12; Indels 34; Gaps 60
QY 1 MURAPPDGLMNASGLAGEAAAGARQFSAAVAVLAALMALLIVATVLAALVMAFV 60
DB 1 MURAPPDGLMNASGLAGEAAAGARQFSAAVAVLAALMALLIVATVLAALVMAFV 60
QY 60 VADSLSRTQNNFFLENAISDFLVCAAPPLDLYVVPVVLTRGWRPSCRLQKRLVAVVLLAT 119
DB 111 LLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLL 119
DB 61 ADSLSRTQNNFFLENAISDFLVCAAPPLDLYVVPVVLTRGWRPSCRLQKRLVAVVLLAT 120
QY 120 SSAPVAVIETLRLSVTKAVSYAGAGLTLRFAVERPRLVAVIATLTYDGLTAWT 129

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AC	AAA09661:
XX	10-AUG-2000 (first entry)
XX	Human histamine H3 receptor cDNA.
XX	Histamine H4 receptor; biogenic amine receptor homologue; ss.
KW	Homo sapiens.
XX	
XX	Key Location/Qualifiers
FH	299..1646
FT	/taag_a
FT	gcgacact histamine_H3_receptor
XX	
XX	W0290020011-A1.
XX	18-APR-2000.
XX	07-OCT-1998; 98w-oDS21999.
PF	
XX	07-OCT-1998; 98w-oDS21999
PR	(ORTH) ORTHO-MCNEIL PHARM INC.
PA	Lorenzberg TW, Erlender M, Hovav A, Pyati J;
P1	WP1: 2000-03363276
XX	p-PSDB: AAY92218.
DE	
PT	Newel human histamine H3 receptor polynucleotides and polypeptides used
XX	in methods to identify modulators of receptor activity
P1	Claim 2: FIG 1A-B; 54pp; English.
PS	
XX	The cDNA encodes the human histamine H3 receptor. The polypeptide
CC	contains the seven conserved hydrophobic domains and specific residues
CC	conserved in biogenic amine receptors. The human histamine H3 receptor
CC	polynucleotides and polypeptides are used in method to screen for
CC	modulators of receptor activity (claimed). Such agonists and antagonists
CC	may prove useful as research tools or may be used as therapeutics to
CC	treat disorders directly or indirectly involving histamine receptors
CC	(claimed). The characterization of the polynucleotide is useful for
CC	forensic analysis, diagnostic applications, and epidemiological studies
XX	
SQ	Sequence 2699 BP; 404 A; 988 C; 805 G; 502 T; 0 other;
Query Match 66.4%; Score 1360.4; DB 21; Length 2699;	
Best Local Similarity 99.9%; Pred. NO. 9,76,229;	
Matches 1461; Conservative 0; Mismatches 1; Indels 0; Gaps 0	
QY	243 tcccaaggcggatgaacctatagaacatatgaagcgacgcgcgccgcagcgaccctaa 302
D6	tcccccaagcggatgaacctatagaacatatgaagcgacgcgcgccgcagcgaccctaa 330
QY	403 caatttcaggggcgtcagagcgacgaagcgacgaagcgacgaagcgacgagctttctgcgc 362
D6	tcccccaagcggatgaacctatagaacatatgaagcgacgcgcgccgcagcgaccctaa 390
QY	463 aaacttcagccgcatctaacgcgcctcatgcgcctcatcatgaacccaactactaaq 422
D6	tcccccaagcggatgaacctatagaacatatgaagcgacgcgcgccgcagcgaccctaa 450
QY	423 caaacctatggagatgaacctatgaacctatgaacctatgaacctatgaacctatga 482
D6	tcccccaagcggatgaacctatagaacatatgaagcgacgcgcgccgcagcgaccctaa 510
QY	483 atttcctgatcaacctgcgcatacttcgaacttctcttcgaagcctttctcacatccactata 542
D6	tcccccaagcggatgaacctatagaacatatgaagcgacgcgcgccgcagcgaccctaa 570
QY	543 ttgacctgcgtgcgttgacgagggcgttatcttcgagagagagctctctgagtagtgccl 602

[illegible]

1


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Db 1081 aqeeatqetqaeatqettttqqetqetqetqqeeceataraeetqetqatqatqatc 1140
QY 1411 eequeeeetareatqeeatqeeetqeeetqeeetqeeetqeeetqeeetqeeetqee 1470
Db 1141 eequeeeetqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqee 1200
QY 1471 eeatqeeaaatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqee 1540
Db 1201 eeatqeeaaatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqee 1260
QY 1541 eequeeteeaaatqeeetqeeetqeeetqeeetqeeetqeeetqeeetqeeetqee 1590
Db 1261 eequeeteeaaatqeeetqeeetqeeetqeeetqeeetqeeetqeeetqeeetqee 1420
QY 1591 aaqeeatqetqaa 1604
Db 1321 aaqeeatqetqaa 1334

RESULT 8
AA009062
Db AAA09062 standard; cDNA; 1335 bp.
Ac
XX
Db 10-AUG-2000 (first entry)
XX
Db Human histamine H3 receptor open reading frame.
XX
KW histamine H3 receptor; biogenic amine receptor; homologue; ss.
XX
OS Homo sapiens.
XX
W0200020011 A1.
Db 13-APR-2000.
XX
P0 07-sep-1998; 98860-0521090.
XX
P1 07-sep-1998; 98860-0521090.
XX
(P010 ) ORTHO MCNEIL PHARM INC.
XX
Lavenberg TW, Erlander M, Hawat A, Pyati J.
XX
WP1; 2000 303642/26.
Db P PS08; AAY92218.
XX
Novel human histamine H3 receptor polynucleotides and polypeptides used
P1 in methods to identify modulators of receptor activity
XX
claim 2; Fig 2; 54pp; English.
XX
The cDNA encodes the human histamine H3 receptor. The polypeptide
Cc contains the seven conserved hydrophobic domains and specific residues
Cc conserved in biogenic amine receptors. The human histamine H3 receptor
Cc polynucleotides and polypeptides are used in methods to screen for
Cc modulators of receptor activity (claimed). Such agonists and antagonists
Cc may prove useful as research tools or may be used as therapeutics to
Cc treat disorders directly or indirectly involving histamine receptors
Cc (claimed). The characterization of the polynucleotide is useful for
Cc forensic analysis, diagnostic applications, and epidemiological studies.
XX
SQ Sequence 1335 bp; 192 A; 47% C; 41% G; 25% T; 0 other;

Query Match
Best Local Similarity 99.9%; Pos. 36; 6,16 224; Length 1335;
Matches 1333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 271 ataaqaaatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqee 330
Db 1 ataaqaaatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqee 60

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QY 441 aaqaaatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqee 300
Db 61 aaqaaatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqee 420
QY 491 ataaqaaatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqee 480
Db 121 ataaqaaatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqee 180
QY 451 aaqaaatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqee 540
Db 181 aaqaaatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqee 240
QY 511 ttaetqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqee 570
Db 241 ttaetqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqee 600
QY 571 aaeeteeaaatqeeetqeeetqeeetqeeetqeeetqeeetqeeetqeeetqeeetqee 640
Db 301 aaeeteeaaatqeeetqeeetqeeetqeeetqeeetqeeetqeeetqeeetqeeetqee 600
QY 631 tetaetqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqee 660
Db 361 tetaetqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqee 420
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Db 421 tetaetqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqee 480
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Db 481 atqetqeeetqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqee 540
QY 811 aaeeteeaaatqeeetqeeetqeeetqeeetqeeetqeeetqeeetqeeetqeeetqee 870
Db 541 aaeeteeaaatqeeetqeeetqeeetqeeetqeeetqeeetqeeetqeeetqeeetqee 600
QY 871 aaeeteeaaatqeeetqeeetqeeetqeeetqeeetqeeetqeeetqeeetqeeetqee 940
Db 601 aaeeteeaaatqeeetqeeetqeeetqeeetqeeetqeeetqeeetqeeetqeeetqee 600
QY 941 atetqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqee 900
Db 661 atetqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqee 720
QY 991 aaqaaatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqee 1050
Db 721 aaqaaatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqee 780
QY 1051 taaqaaatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqee 1110
Db 781 taaqaaatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqee 840
QY 1111 aaqaaatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqee 1170
Db 841 aaqaaatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqee 900
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Db 901 aaqaaatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqee 960
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Db 961 aaqaaatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqee 1020
QY 1291 tetaetqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqee 1350
Db 1021 tetaetqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqee 1080
QY 1351 aaqaaatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqee 1410
Db 1081 aaqaaatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqeeatqee 1140

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